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RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/10/042,211A

TIME: 13:24:54

Input Set : D:\1254-0192P_SequenceListing.txt

Output Set: N:\CRF3\06032002\J042211A.raw

3 <110> APPLICANT: MATSUDA, Akio et al.
 5 <120> TITLE OF INVENTION: NFKB Activating Gene
 7 <130> FILE REFERENCE: 1254-0192P
 9 <140> CURRENT APPLICATION NUMBER: US 10/042,211A
 10 <141> CURRENT FILING DATE: 2002-01-11
 12 <150> PRIOR APPLICATION NUMBER: JP 2000-402288
 13 <151> PRIOR FILING DATE: 2000-12-28
 15 <150> PRIOR APPLICATION NUMBER: JP 2001-088912
 16 <151> PRIOR FILING DATE: 2001-03-26
 18 <150> PRIOR APPLICATION NUMBER: JP 2001-254018
 19 <151> PRIOR FILING DATE: 2001-08-24
 21 <150> PRIOR APPLICATION NUMBER: US 60/258,315
 22 <151> PRIOR FILING DATE: 2000-12-28
 24 <150> PRIOR APPLICATION NUMBER: US 60/278,640
 25 <151> PRIOR FILING DATE: 2001-03-26
 27 <150> PRIOR APPLICATION NUMBER: US 60/314,385
 28 <151> PRIOR FILING DATE: 2001-08-24
 30 <160> NUMBER OF SEQ ID NOS: 182
 32 <170> SOFTWARE: PatentIn Ver. 2.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 167
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Homo sapiens
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 41 1 5 10 15
 43 Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr
 44 20 25 30
 46 Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
 47 35 40 45
 49 Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
 50 50 55 60
 52 Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
 53 65 70 75 80
 55 Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
 56 85 90 95
 58 Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
 59 100 105 110
 61 Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
 62 115 120 125
 64 Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
 65 130 135 140
 67 Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly

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70 Tyr Gly Gly Thr Arg Arg Arg
71          165
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 1472
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapiens
79 <220> FEATURE:
80 <221> NAME/KEY: CDS
81 <222> LOCATION: (194)..(694)
83 <400> SEQUENCE: 2
84 aaaaactgtg gtgagctgtg aaggctatga gtcctctgaa gaccagtatg tactaagagg 60
86 ttcttgtggc ttggagtata atttagatta tacagaactt ggcctgcaga aactgaagga 120
88 gtctgaaaag cagcacggct ttgcctcttt ctctgattat tattataagt ggctctcggc 180
90 ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg 229
91          Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
92          1          5          10
94 atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277
95 Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
96          15          20          25
98 cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325
99 Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
100          30          35          40
102 ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373
103 Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe
104 45          50          55          60
106 aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421
107 Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser
108          65          70          75
110 gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469
111 Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
112          80          85          90
114 aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517
115 Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
116          95          100          105
118 aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565
119 Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
120          110          115          120
122 ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga 613
123 Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
124 125          130          135          140
126 ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga 661
127 Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
128          145          150          155
130 act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714
131 Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
132          160          165
134 aaacactgga tgcagaaatt ttggattttt catcacttcc tcttttagaaa aaaagtacta 774
136 cctgttaaca attgggaaaa ggggatattc aaaagttcgg tgggtgttatg tccagtgtag 834

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138 ctttttgtat tctattatatt gagggctaaaa gttgatgtgt gacaaaatac ttatgtgttg 894
140 tatgtcagtg taacatgcag atgtatattg cagtttttga aagtgatcat tactgtggaa 954
142 tgctaaaaaat acattaatatt ctaaaacctg tgatgcccta agaagcatta agaatgaagg 1014
144 tgttgtaacta atagaaaacta agtacagaaa atttcagttt taggtggttg tagctgatga 1074
146 gttattacct catagagact gtaatatattt atttggtatt atattatttg atgtttgctg 1134
148 ttcttcaaac atttaaatca agctttggac taattatgct aatttgtgag ttctgatcac 1194
150 ttttgagctc tgaagctttg aatcattcag tgggtggagat ggccttctgg taactgaata 1254
152 ttaccttctg taggaaaagg tggaaaataa gcatctagaa ggttggttg atgactctg 1314
154 tgctggcaaaa aatgcttgaa acctctatat ttctttcgtt cataagaggt aaaggtcaaa 1374
156 tttttcaaca aaagtctttt aataacaaaa gcatgcagtt ctctgtgaaa tctcaaatat 1434
158 tgttgtaata gtctgtttca atcttaaaaa gaatcaat 1472
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 339
163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 3
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170 Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
171 20 25 30
173 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
174 35 40 45
176 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
177 50 55 60
179 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
180 65 70 75 80
182 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
183 85 90 95
185 Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
186 100 105 110
188 Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
189 115 120 125
191 Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
192 130 135 140
194 Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
195 145 150 155 160
197 Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
198 165 170 175
200 Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
201 180 185 190
203 Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
204 195 200 205
206 Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
207 210 215 220
209 Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
210 225 230 235 240
212 Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
213 245 250 255
215 Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

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216          260          265          270
218 Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
219          275          280          285
221 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
222          290          295          300
224 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
225 305          310          315          320
227 Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
228          325          330          335
230 Arg Arg Arg
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 1924
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (115)..(1131)
243 <400> SEQUENCE: 4
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246 ccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117
247                                     Met
248                                     1
250 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
251 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Gly
252          5          10          15
254 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
255 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
256          20          25          30
258 cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
259 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
260          35          40          45
262 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
263 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
264 50          55          60          65
266 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
267 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
268          70          75          80
270 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
271 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
272          85          90          95
274 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
275 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
276          100          105          110
278 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
279 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
280          115          120          125
282 tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
283 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
284 130          135          140          145

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286 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
287 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
288      150      155      160
290 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
291 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
292      165      170      175
294 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
295 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
296      180      185      190
298 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
299 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
300      195      200      205
302 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
303 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
304 210      215      220      225
306 cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
307 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
308      230      235      240
310 gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
311 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
312      245      250      255
314 aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
315 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
316      260      265      270
318 gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
319 Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
320      275      280      285
322 tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029
323 Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
324 290      295      300      305
326 gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
327 Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
328      310      315      320
330 aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
331 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
332      325      330      335
334 aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt 1181
335 Arg Arg
337 catcactttc tctttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc 1241
339 aaaagttcgg tgggtgtatg tccagtgtag ctttttgtat tctattattt gaggctaaaa 1301
341 gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg 1361
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347 atttcagttt taggtggttg tagctgatga gttattacct catagagact gtaatattct 1541
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